

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.
Shah, Purvi

(ii) TITLE OF THE INVENTION: NEW HUMAN PHOSPHATIDYLINOSITOL
(4,5) BISPHOSPHATE 5-PHOSPHATASE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Genomics, Inc.
(B) STREET: 3160 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/258,643; 08/884,681
(B) FILING DATE: February 26, 1999; June 27, 1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Eckstrom, Richard A.
(B) REGISTRATION NUMBER: 37,027
(C) REFERENCE/DOCKET NUMBER: PF-0334-2 DIV

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRSTNOT03
(B) CLONE: 638789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Val	Leu	Ser	Pro	Leu	Ser	Phe	Ile	Lys	Val	Ser	His	Val	Arg
1				5					10					15	
Met	Gln	Gly	Ile	Leu	Leu	Leu	Val	Phe	Ala	Lys	Tyr	Gln	His	Leu	Pro
				20				25						30	
Tyr	Ile	Gln	Ile	Leu	Ser	Thr	Lys	Ser	Thr	Pro	Thr	Gly	Leu	Phe	Gly
				35				40						45	
Tyr	Trp	Gly	Asn	Lys	Gly	Gly	Val	Asn	Ile	Cys	Leu	Lys	Leu	Tyr	Gly

50 55 60
Tyr Tyr Val Ser Ile Ile Asn Cys His Leu Pro Pro His Ile Ser Asn
65 70 75
Asn Tyr Gln Arg Leu Glu His Phe Asp Arg Ile Leu Glu Met Gln Asn
80 85 90 95
Cys Glu Gly Arg Asp Ile Pro Asn Ile Leu Asp His Asp Leu Ile Ile
100 105 110
Trp Phe Gly Asp Met Asn Phe Arg Ile Glu Asp Phe Gly Leu His Phe
115 120 125
Val Arg Glu Ser Ile Lys Asn Arg Cys Tyr Gly Gly Leu Trp Glu Lys
130 135 140
Asp Gln Leu Ser Ile Ala Lys Lys His Asp Pro Leu Leu Arg Glu Phe
145 150 155 160
Gln Glu Gly Arg Leu Leu Phe Pro Pro Thr Tyr Lys Phe Asp Arg Asn
165 170 175
Ser Asn Asp Tyr Asp Thr Ser Glu Lys Lys Arg Lys Pro Ala Trp Thr
180 185 190
Asp Arg Ile Leu Trp Arg Leu Lys Arg Gln Pro Cys Ala Gly Pro Asp
195 200 205
Thr Pro Ile Pro Pro Ala Ser His Phe Ser Leu Ser Leu Arg Gly Tyr
210 215 220
Ser Ser His Met Thr Tyr Gly Ile Ser Asp His Lys Pro Val Ser Gly
225 230 235 240
Thr Phe Asp Leu Glu Leu Lys Pro Leu Val Ser Ala Pro Leu Ile Val
245 250 255
Leu Met Pro Glu Asp Leu Trp Thr Val Glu Asn Asp Met Met Val Ser
260 265 270
Tyr Ser Ser Thr Ser Asp Phe Pro Ser Ser Pro Trp Asp Trp Ile Gly
275 280 285
Leu Tyr Lys Val Gly Leu Arg Asp Val Asn Asp Tyr Val Ser Tyr Ala
290 295 300
Trp Val Gly Asp Ser Lys Val Ser Cys Ser Asp Asn Leu Asn Gln Val
305 310 315 320
Tyr Ile Asp Ile Ser Asn Ile Pro Thr Trp Glu Asp Glu Phe Leu Leu
325 330 335
Cys Tyr Tyr Ser Asn Ser Leu Arg Ser Val Val Gly Ile Ser Arg Pro
340 345 350
Phe Gln Ile Pro Pro Gly Ser Leu Arg Glu Asp Pro Leu Gly Glu Ala
355 360 365
Gln Pro Gln Ile
370

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
(B) CLONE: 638789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAAGGCTCAG	CATACACGTC	GTGACTTGGA	ACGTGGCTTC	GCAGCGCCCC	CTCAGGCTCT	60
CAGTGACCTG	CTTCAGCTGA	ACAACCGGAA	CCTCAATCTT	GACATATATG	TTATTTGGTTT	120
GCAGGAATTG	AACTCTGGGA	TCATAAGCCT	CTTTCCGAT	GCATGCCCTTA	ATGACTGCTG	180
GAGCAGTTTC	TCATGGATG	TGCTTTCCCC	TCAGGCTTC	ATCAAGGTCT	CCCATGTCGG	240
TATGCAGGGG	ATCCTCTTAC	TGGTCTTTGC	CAAGTATCAG	CATTTGCCCT	ATATCCAGAT	300
TCTGTCTACT	AAATCCACCC	CCACTGGCCT	GTTTGGGTAC	TGGGGGAACA	AAGGTGGAGT	360
CAACATCTGC	CTGAAGCTTT	ATGGCTACTA	TGTGAGCATC	ATCAACTGCC	ACCTGCTCTC	420
CCACATTTCC	AACAATTACC	AGCGGCTGGA	GCACTTTGAC	CGGATCCCTGG	AGATGCAGAA	480
TTGTGAGGGG	CGAGACATCC	CAACATCTCT	GGACCACGAC	CTCATTATCT	GGTTTGGAGA	540
CATGAACCTT	CGGATCGAGG	ACTTTGGGTT	GCACTTTGTT	CGGGAATCCA	TAAAAAATCG	600

GTGCTACGGT GGCCGTGTGG AGAAGGACCA GCTCAGCATT GCCAAGAANA ATGACCCGCT 560
 GCTCCGGGAG TTCCAGGAGG GCCGCCCTACT CTTCGCCGCC ACCTACAAGT TTGATAGGAA 720
 CTCACACGAC TATGACACCA GTGAGAAAAA ACGCAAGCCT GCATGGACCG ATCGCATCTCT 780
 GTGAGGCTG AAGCGGCAGC CCTGTGCTGG CCCCAGACCT CCCATACCGG CGGCGTCACA 840
 CTTCTCCTTG TCCTGTAGGG GCTACAGCAG CCACATGACG TACGGCATCA GCGACACCAA 900
 GCCGTGCTCC GGCACGTTTC ACTTGGAGCT GAAGCCATTG GTGCTGTCTC CGCTGATCGT 960
 CCTGATGCCG GAGGACCTGT GGACCGTGA AATGACATG ATGGTTCAGCT ACTCTTCAAC 1020
 CTGCGACTTC CCCACGACG CGTGGGACTG GATTGGACTG TACAAGGTGG GCGTCGGGGA 1080
 CGTTAATGAC TACGTGTCTT ATGCCTGGGT CGGGGACAGC AAGGTCTCTT GCACGACAAA 1140
 CTTGAACACG GTTTACATCG ACATCAGCAA TATCCCTACC ACTGAAGATG AGTTTCTCTCT 1200
 CCGTTACTAC AGCAACAGTC TGCGTTCTGT GTTGGGGATA AGCAGACCTT TCCAGATCCC 1260
 GCGTGTGCTC TTGAGGGAGG ACCCACTGGG TGAAGCAGAG CCACAGATCT GAGCGAGGAT 1320
 GGGAGTGAAT CCCAGCGCGA GGCAGAGGCT GGCAGCAGC TGTGCTTTTC CACTGCGGGG 1380
 AGTGTGCGGG GCGCCAGCTG GCCCCGTGAA GAGACAGCCA AGTGTCTGTC ACATACTCTCT 1440
 CCGAGAGTGA GCTCTAACCA GGCCTATTTC CTCTCTCCAC TACTCATCTC TGAATTTAGC 1500
 CGCTTAATAA CAGGTTTTTG TTGCTGAGAT GTGAGTGA AA CCAGCTAGTG TTCTCAACAGT 1560
 GAAGACCTGG GAGACGTTCT GCGTCTCAT TCTGTATGCC TACCCCTCTT TCTAGTCTTG 1620
 CCTAAGTAGT CTTGCCAGCG ACATGCCCAA TTTGGCAGAG GCGTGCATTC TTGCTGTGCC 1680
 GTCTCTGGCC TACAGCTGTC TGGGAGGGGA GATGCTCACA TTTGTACAGG CTACATAGAC 1740
 TGTGTCAAGC AGTGTGTGAT TCCAGGAGTC TTGGCATCTC ATAGCTTGTC CCCGTGAGGA 1800
 GTGAGACGAG GGTCTGGGAT TTCTGCTTTT AGCAAAAAGA GTCTGACTCA GTGGGACAAA 1860
 TGGAGGGGCC CCTCTAGCCA GGCTCTTAGC CCATGTTTAT GAGCAGGTG ATGAGGGTCC 1920
 TTCGGCCAGC ACAAGCTTTC TCCCTACTCA CGGCATGGAG TCTGACTGCA TGGAAATGCC 1980
 AGATCTCGAG AGAGAGGATC GGAAGAGGAT CAGGTTTCGT TCCGTGGTA GCTTGAGTCC 2040
 CATGCTTCCA CCTGCCATC TGAGGAAGGG GTGACAAGTG GTCAAGGAGC TGTGGCCACA 2100
 GACTTTTCCA GGGTGGTCTT TGCGAGGTGA GGTGCGTCTG TGCCACCTTT GTCAGGAGTC 2160
 ATTGTACGAG GCGCCCCCTT GGACCCCGCG GACCTCAGA GTGGGGGCGG GCAGAAGGGA 2220
 GAACACAGTC AAGACATTTT GGAGGATCTG GCCTTGGGT TCTTCAGAGA ACACCTCTTA 2280
 GGGGCTTTGG GGACATGGCC TGTCCCCACA TCCAGCACTT GCCTCCGCCA TGCTCACTCG 2340
 CGAGCCCTTT TCCAGGAGA AGACACCTCT GGGAGCCTGC TCAGTGTCTG TCTCGGCATC 2400
 TGTGTCTCTT GGACTTGAGG TTACTCCAGT TGCTCTGTGT TGCTACTCTT CCCCCCAAG 2460
 CCTGTGTATG AAGAATTGTC CCTTGGCTTC CAGCAGGCCA TGCGTGGCTG TTTTGTGACT 2520
 GTTACATTGT GCAGGGGTAA TTATTAGCGT GGCTTTTACA CTPTAAAAAA AAA 2573

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1399101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Gly Leu Phe Gly Tyr Trp Gly Asn Lys Gly Gly Val Asn Ile Cys
 1 5 10 15
 Leu Lys Leu Tyr Gly Tyr Tyr Val Ser Ile Ile Asn Cys His Leu Pro
 20 25 30
 Pro His Ile Ser Asn Asn Tyr Gln Arg Leu Glu His Phe Asp Arg Ile
 35 40 45
 Leu Glu Met Gln Asn Cys Glu Gly Arg Asp Ile Pro Asn Ile Leu Asp
 50 55 60
 His Asp Leu Ile Ile Trp Phe Gly Asp Met Asn Phe Arg Ile Glu Asp
 65 70 75 80
 Phe Gly Leu His Phe Val Arg Glu Ser Ile Lys Asn Arg Cys Tyr Gly
 85 90 95
 Gly Leu Trp Glu Lys Asp Gln Leu Ser Ile Ala Lys Lys His Asp Pro
 100 105 110
 Leu Leu Arg Glu Phe Gln Glu Gly Arg Leu Leu Phe Pro Pro Thr Tyr
 115 120 125
 Lys Phe Asp Arg Asn Ser Asn Asp Tyr Asp Thr Ser Glu Lys Lys Arg

130 135 140
 Lys Pro Ala Trp Thr Asp Arg Ile Leu Trp Arg Leu Lys Arg Gln Pro
 145 150 155 160
 Cys Ala Gly Pro Asp Thr Pro Ile Pro Pro Ala Ser His Phe Ser Leu
 165 170 175
 Ser Leu Arg Gly Tyr Ser Ser His Met Thr Tyr Gly Ile Ser Asp His
 180 185 190
 Lys Pro Val Ser Gly Thr Phe Asp Leu Glu Leu Lys Pro Leu Val Ser
 195 200 205
 Ala Pro Leu Ile Val Leu Met Pro Glu Asp Leu Trp Thr Val Glu Asn
 210 215 220
 Asp Met Met Val Ser Tyr Ser Ser Thr Ser Asp Phe Pro Ser Ser Pro
 225 230 235 240
 Trp Asp Trp Ile Gly Leu Tyr Lys Val Gly Leu Arg Asp Val Asn Asp
 245 250 255
 Tyr Val Ser Tyr Ala Trp Val Gly Asp Ser Lys Val Ser Cys Ser Asp
 260 265 270
 Asn Leu Asn Gln Val Tyr Ile Asp Ile Ser Asn Ile Pro Thr Thr Glu
 275 280 285
 Asp Glu Phe Leu Leu Cys Tyr Tyr Arg Asn Ser Leu Arg Ser Val Val
 290 295 300
 Gly Ile Arg Arg Pro Phe Gln Ile Pro Pro Gly Ser Leu Arg Glu Asp
 305 310 315 320
 Pro Leu Gly Glu Ala Gln Pro Gln Ile
 325

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1019103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Thr Val Pro Glu Pro Gly Ala Ala Glu Ser Arg Ala Pro Cys Gly
 1 5 10 15
 Asp Ser Ser Gly Gly Cys Val Arg Ser Ala Gly Ala Ser Met Asp Gln
 20 25 30
 Ser Val Ala Ile Gln Glu Thr Leu Ala Glu Gly Glu Tyr Cys Val Ile
 35 40 45
 Ala Val Gln Gly Val Leu Cys Glu Gly Asp Ser Arg Gln Ser Arg Leu
 50 55 60
 Leu Gly Leu Val Arg Tyr Arg Leu Glu His Gly Gly Gln Glu His Ala
 65 70 75 80
 Leu Phe Leu Tyr Thr His Arg Arg Met Ala Ile Thr Gly Asp Asp Val
 85 90 95
 Ser Leu Asp Gln Ile Val Pro Val Ser Arg Asp Phe Thr Leu Glu Glu
 100 105 110
 Val Ser Pro Asp Gly Glu Leu Tyr Ile Leu Gly Ser Asp Val Thr Val
 115 120 125
 Gln Leu Asp Thr Ala Glu Leu Ser Leu Val Phe Gln Leu Pro Phe Gly
 130 135 140
 Ser Gln Thr Arg Met Phe Leu His Glu Val Ala Arg Ala Cys Pro Gly
 145 150 155 160
 Phe Asp Ser Ala Thr Arg Asp Pro Glu Phe Leu Trp Leu Ser Arg Tyr
 165 170 175
 Arg Cys Ala Glu Leu Glu Leu Glu Met Pro Thr Pro Arg Gly Cys Asn
 180 185 190
 Ser Ala Leu Val Thr Trp Pro Gly Tyr Ala Thr Ile Gly Gly Gly Gly
 195 200 205

Ser Asn Phe Asp Gly Leu Arg Pro Asn Gly Lys Gly Val Pro Met Asp
 210 215 220
 Gln Ser Ser Arg Gly Gln Asp Lys Pro Glu Ser Leu Gln Pro Arg Gln
 225 230 235 240
 Asn Lys Ser Lys Ser Glu Ile Thr Asp Met Val Arg Ser Ser Thr Ile
 245 250 255
 Thr Val Ser Asp Lys Ala His Ile Leu Ser Met Gln Lys Phe Gly Leu
 260 265 270
 Arg Asp Thr Ile Val Lys Ser His Leu Leu Gln Lys Glu Glu Asp Tyr
 275 280 285
 Thr Tyr Ile Gln Asn Phe Arg Phe Phe Ala Gly Thr Tyr Asn Val Asn
 290 295 300
 Gly Gln Ser Pro Lys Glu Cys Leu Arg Leu Trp Leu Ser Asn Gly Ile
 305 310 315 320
 Gln Ala Pro Asp Val Tyr Cys Val Gly Phe Gln Glu Leu Asp Leu Ser
 325 330 335
 Lys Glu Ala Phe Phe Phe His Asp Thr Pro Lys Glu Glu Glu Trp Phe
 340 345 350
 Lys Ala Val Ser Glu Gly Leu His Pro Asp Ala Lys Tyr Ala Lys Val
 355 360 365
 Lys Leu Ile Arg Leu Val Gly Ile Met Leu Leu Leu Tyr Val Lys Gln
 370 375 380
 Glu His Ala Ala Tyr Ile Ser Glu Val Glu Ala Glu Thr Val Gly Thr
 385 390 395 400
 Gly Ile Met Gly Arg Met Gly Asn Lys Gly Gly Val Ala Ile Arg Phe
 405 410 415
 Gln Phe His Asn Thr Ser Ile Cys Val Val Asn Ser His Leu Ala Ala
 420 425 430
 His Ile Glu Glu Tyr Glu Arg Arg Asn Gln Asp Tyr Lys Asp Ile Cys
 435 440 445
 Ser Arg Met Gln Phe Cys Gln Pro Asp Pro Ser Leu Pro Pro Leu Thr
 450 455 460
 Ile Ser Asn His Asp Val Ile Leu Trp Leu Gly Asp Leu Asn Tyr Arg
 465 470 475 480
 Ile Glu Glu Leu Asp Val Glu Lys Val Lys Leu Ile Glu Glu Lys
 485 490 495
 Asp Phe Gln Met Leu Tyr Ala Tyr Asp Gln Leu Lys Ile Gln Val Ala
 500 505 510
 Ala Lys Thr Val Phe Glu Gly Phe Thr Glu Gly Glu Leu Thr Phe Gln
 515 520 525
 Pro Thr Tyr Lys Tyr Asp Thr Gly Ser Asp Asp Trp Asp Thr Ser Glu
 530 535 540
 Lys Cys Arg Ala Pro Ala Trp Cys Asp Arg Ile Leu Trp Lys Gly Lys
 545 550 555 560
 Asn Ile Thr Gln Leu Ser Tyr Gln Ser His Met Ala Leu Lys Thr Ser
 565 570 575
 Asp His Lys Pro Val Ser Ser Val Phe Asp Ile Gly Val Arg Val Val
 580 585 590
 Asn Asp Glu Leu Tyr Arg Lys Thr Leu Glu Glu Ile Val Arg Ser Leu
 595 600 605
 Asp Lys Met Glu Asn Ala Asn Ile Pro Ser Val Ser Leu Ser Lys Arg
 610 615 620
 Glu Phe Cys Phe Gln Asn Val Lys Tyr Met Gln Leu Lys Val Glu Ser
 625 630 635 640
 Phe Thr Ile His Asn Gly Gln Val Pro Cys His Phe Glu Phe Ile Asn
 645 650 655
 Lys Pro Asp Glu Glu Ser Tyr Cys Lys Gln Trp Leu Asn Ala Asn Pro
 660 665 670
 Ser Arg Gly Phe Leu Leu Pro Asp Ser Asp Val Glu Ile Asp Leu Glu
 675 680 685
 Leu Phe Val Asn Lys Thr Thr Ala Thr Lys Leu Asn Ser Gly Glu Asp
 690 695 700
 Lys Ile Glu Asp Ile Leu Val Leu His Leu Asp Arg Gly Lys Asp Tyr
 705 710 715 720
 Phe Leu Ser Val Ser Gly Asn Tyr Leu Pro Ser Cys Phe Gly Ser Pro
 725 730 735

```

Ile His Thr Leu Cys Tyr Met Arg Glu Pro Ile Leu Asp Leu Pro Leu
740 745 750
Glu Thr Ile Ser Glu Leu Thr Leu Met Pro Val Trp Thr Gly Asp Asp
755 760 765
Gly Ser Gln Leu Asp Ser Pro Met Glu Ile Pro Lys Glu Leu Trp Met
770 775 780
Met Val Asp Tyr Leu Tyr Arg Asn Ala Val Gln Gln Glu Asp Leu Phe
785 790 795 800
Gln Gln Pro Gly Leu Arg Ser Glu Phe Glu His Ile Arg Asp Cys Leu
805 810 815
Asp Thr Gly Met Ile Asp Asn Leu Ser Ala Ser Asn His Ser Val Ala
820 825 830
Glu Ala Leu Leu Leu Phe Leu Glu Ser Leu Pro Glu Pro Val Ile Cys
835 840 845
Tyr Ser Thr Tyr His Asn Cys Leu Glu Cys Ser Gly Asn Tyr Thr Ala
850 855 860
Ser Lys Gln Val Ile Ser Thr Leu Pro Ile Phe His Lys Asn Val Phe
865 870 875 880
His Tyr Leu Met Ala Phe Leu Arg Glu Leu Leu Lys Asn Ser Ala Lys
885 890 895
Asn His Leu Asp Glu Asn Ile Leu Ala Ser Ile Phe Gly Ser Leu Leu
900 905 910
Leu Arg Asn Pro Ala Gly His Gln Lys Leu Asp Met Thr Glu Lys Lys
915 920 925
Lys Ala Gln Glu Phe Ile His Gln Phe Leu Cys Asn Pro Leu
930 935 940

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1420920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Glu Pro Pro Leu Pro Val Gly Ala Gln Pro Leu Ala Thr Val Glu
1 5 10 15
Gly Met Glu Met Lys Gly Pro Leu Arg Glu Pro Cys Ala Leu Thr Leu
20 25 30
Ala Gln Arg Asn Gly Gln Tyr Glu Leu Ile Ile Gln Leu His Glu Lys
35 40 45
Glu Gln His Val Gln Asp Ile Ile Pro Ile Asn Ser His Phe Arg Cys
50 55 60
Val Gln Glu Ala Glu Glu Thr Leu Leu Ile Asp Ile Ala Ser Asn Ser
65 70 75 80
Gly Cys Lys Ile Arg Val Gln Gly Asp Trp Ile Arg Glu Arg Arg Phe
85 90 95
Glu Ile Pro Asp Glu Glu His Cys Leu Lys Phe Leu Ser Ala Val Leu
100 105 110
Ala Ala Gln Lys Ala Gln Ser Gln Leu Leu Val Pro Glu Gln Lys Asp
115 120 125
Ser Ser Ser Trp Tyr Gln Lys Leu Asp Thr Lys Asp Lys Pro Ser Val
130 135 140
Phe Ser Gly Leu Leu Gly Phe Glu Asp Asn Phe Ser Ser Met Asn Leu
145 150 155 160
Asp Lys Lys Ile Asn Ser Gln Asn Gln Pro Thr Gly Ile His Arg Glu
165 170 175
Pro Pro Pro Pro Phe Ser Val Asn Lys Met Leu Pro Arg Glu Lys
180 185 190
Glu Ala Ser Asn Lys Glu Gln Pro Lys Val Thr Asn Thr Met Arg Lys

```

58

59